STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/554,372

Source: TRWP

Date Processed by STIC: 4/27/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: /O/SS4,372

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____ Variable Length — Sequence(s)____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
. (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

RAW SEQUENCE LISTING   DATE: 04/27/2007
PATENT APPLICATION: US/10/554,372   TIME: 11:42:58

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272007\J554372.raw

```
    3 <110> APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
    5 <120> TITLE OF INVENTION: Beta-amyloid inhibitors and use thereof
    7 <130> FILE REFERENCE: WO/850
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/554,372
C-->  9 <141> CURRENT FILING DATE: 2005-10-25
    9 <160> NUMBER OF SEQ ID NOS: 11
   11 <170> SOFTWARE: PatentIn version 3.1
   13 <210> SEQ ID NO: 1
   14 <211> LENGTH: 7
   15 <212> TYPE: PRT
   16 <213> ORGANISM: synthetic construct
   18 <220> FEATURE:
   19 <221> NAME/KEY: MISC_FEATURE
   20 <222> LOCATION: (1)..(1)
   21 <223> OTHER INFORMATION: X can be absent or is an acetyl group
   24 <220> FEATURE:
   25 <221> NAME/KEY: MISC_FEATURE
   26 <222> LOCATION: (2)..(2)
   27 <223> OTHER INFORMATION: X is the following fragment [Lys X2 X3 Phe Gln]m
wherein X2 is selected
   28       from Ile and Leu and X3 is selected from Pro and Trp. m is an integer
selected
   29       from 0 and 1.
   32 <220> FEATURE:
   33 <221> NAME/KEY: MISC_FEATURE
   34 <222> LOCATION: (6)..(6)
   35 <223> OTHER INFORMATION: X is the following fragment [Lys X4 Pro Phe Gln]n
wherein X4 is selected
   36       from Ile and Leu. n is an integer selected from 1 and 2.
   39 <220> FEATURE:
   40 <221> NAME/KEY: MISC_FEATURE
   41 <222> LOCATION: (7)..(7)
   42 <223> OTHER INFORMATION: X is a peptidic moiety of a length selected from
1, 2, 3, 4, 5, 6, 7 and
   43       8 and containing at least one basic amino acid and which is amidated
at the C-
   44       terminus
   47 <400> SEQUENCE: 1
W--> 49 Xaa Xaa Arg Gln Ile Xaa Xaa
   50 1               5
   53 <210> SEQ ID NO: 2
   54 <211> LENGTH: 8
   55 <212> TYPE: PRT
   56 <213> ORGANISM: synthetic construct
```

Handwritten annotations: "Invalid response — See item #10 on error summary sheet."; "Does Not Comply Corrected Diskette Needed (pgs. 1-6)"; "See item #10 on error summary sheet. FYI, See item #13 on error summary sheet."; "Same error"

```
58 <220> FEATURE:
59 <221> NAME/KEY: MISC_FEATURE
60 <222> LOCATION: (2)..(2)
61 <223> OTHER INFORMATION: X is selected from Arg and Lys.
```

```
 64 <220> FEATURE:
 65 <221> NAME/KEY: MISC_FEATURE
 66 <222> LOCATION: (3)..(3)
 67 <223> OTHER INFORMATION: X is selected from Arg and Lys.
 70 <220> FEATURE:
 71 <221> NAME/KEY: MISC_FEATURE
 72 <222> LOCATION: (5)..(5)
 73 <223> OTHER INFORMATION: X is selected from Arg and Lys.
 76 <220> FEATURE:
 77 <221> NAME/KEY: MISC_FEATURE
 78 <222> LOCATION: (7)..(7)
 79 <223> OTHER INFORMATION: X is selected from Arg and Lys.
 82 <220> FEATURE:
 83 <221> NAME/KEY: MISC_FEATURE
 84 <222> LOCATION: (8)..(8)
 85 <223> OTHER INFORMATION: X is selected from amidated Arg and amidated Lys.
 88 <400> SEQUENCE: 2
```
W--> 90 **Asn Xaa Xaa Met Xaa Trp Xaa Xaa**
```
 91 1                 5
 94 <210> SEQ ID NO: 3
 95 <211> LENGTH: 7
 96 <212> TYPE: PRT
 97 <213> ORGANISM: synthetic construct
 99 <220> FEATURE:
100 <221> NAME/KEY: MISC_FEATURE
101 <222> LOCATION: (1)..(1)
102 <223> OTHER INFORMATION: X can be absent or is an acetyl group
105 <220> FEATURE:
106 <221> NAME/KEY: MISC_FEATURE
107 <222> LOCATION: (2)..(2)
108 <223> OTHER INFORMATION: X is the following fragment [Lys X2 X3 Phe Gln]m
wherein X2 is selected
109         from Ile and Leu and X3 is selected from Pro and Trp. m is an
integer selected
110         from 0 and 1.
113 <220> FEATURE:
114 <221> NAME/KEY: MISC_FEATURE
115 <222> LOCATION: (6)..(6)
116 <223> OTHER INFORMATION: X is the following fragment [Lys X4 X5 Phe Gln]n
wherein X4 is selected
117         from Ile and Leu, X5 is selected from Pro and Trp. n is an integer
selected from
118         1 and 2.
121 <220> FEATURE:
122 <221> NAME/KEY: MISC_FEATURE
123 <222> LOCATION: (7)..(7)
124 <223> OTHER INFORMATION: X is a peptidic moiety of a length selected from
1, 2, 3, 4, 5, 6, 7 and
125         8 and containing at least one basic amino acid and which is amidated
at the C-
126         terminus.
129 <400> SEQUENCE: 3
```
W--> 131 **Xaa Xaa Arg Gln Ile Xaa Xaa**

(handwritten annotations:) same error — see item # 10 on error summary Sheet

(handwritten annotation:) FYI, See item #13 on error summary Sheet

```
132 1                    5
135 <210> SEQ ID NO: 4
```

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\04272007\J554372.raw**

SAME errors

```
     136 <211> LENGTH: 16
     137 <212> TYPE: PRT
     138 <213> ORGANISM: synthetic construct
     140 <220> FEATURE:
     141 <221> NAME/KEY: MISC_FEATURE
     142 <222> LOCATION: (16)..(16)
     143 <223> OTHER INFORMATION: X is amidated Lysine
     146 <400> SEQUENCE: 4
W--> 148 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Xaa
     149 1               5                   10                  15
     152 <210> SEQ ID NO: 5
     153 <211> LENGTH: 5
     154 <212> TYPE: PRT
     155 <213> ORGANISM: synthetic construct
     157 <220> FEATURE:
     158 <221> NAME/KEY: MISC_FEATURE
     159 <222> LOCATION: (1)..(1)
     160 <223> OTHER INFORMATION: X is Acetylated Leucine
     163 <220> FEATURE:
     164 <221> NAME/KEY: MISC_FEATURE
     165 <222> LOCATION: (5)..(5)
     166 <223> OTHER INFORMATION: X is amidated aspartic acid
     169 <400> SEQUENCE: 5
W--> 171 Xaa Pro Phe Phe Xaa
     172 1               5
     175 <210> SEQ ID NO: 6
     176 <211> LENGTH: 21
     177 <212> TYPE: PRT
     178 <213> ORGANISM: synthetic construct
     180 <220> FEATURE:
     181 <221> NAME/KEY: MISC_FEATURE
     182 <222> LOCATION: (21)..(21)
     183 <223> OTHER INFORMATION: X is amidated Aspartic Acid
     186 <400> SEQUENCE: 6
     188 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
     189 1               5                   10                  15
W--> 192 Leu Pro Phe Phe Xaa
     193             20
     196 <210> SEQ ID NO: 7
     197 <211> LENGTH: 16
     198 <212> TYPE: PRT
     199 <213> ORGANISM: synthetic construct
     201 <220> FEATURE:
     202 <221> NAME/KEY: MISC_FEATURE
     203 <222> LOCATION: (1)..(1)
     204 <223> OTHER INFORMATION: X is acetylated Arginine.
     207 <220> FEATURE:
     208 <221> NAME/KEY: MISC_FEATURE
     209 <222> LOCATION: (16)..(16)
```

```
      210 <223> OTHER INFORMATION: X is amidated amidate Lysine.
      213 <400> SEQUENCE: 7
W--> 215 Xaa Gln Ile Lys Ile Pro Phe Gln Asn Arg Arg Met Lys Trp Lys Xaa
      216 1               5                   10                  15
      219 <210> SEQ ID NO: 8
      220 <211> LENGTH: 21
      221 <212> TYPE: PRT
      222 <213> ORGANISM: synthetic construct
      224 <220> FEATURE:
      225 <221> NAME/KEY: MISC_FEATURE
      226 <222> LOCATION: (1)..(1)
      227 <223> OTHER INFORMATION: X is acetylated Arginine.
      230 <220> FEATURE:
      231 <221> NAME/KEY: MISC_FEATURE
      232 <222> LOCATION: (21)..(21)
      233 <223> OTHER INFORMATION: X is amidated Lysine.
      236 <400> SEQUENCE: 8
W--> 238 Xaa Gln Ile Lys Ile Pro Phe Gln Lys Ile Pro Phe Gln Asn Arg Arg
      239 1               5                   10                  15
      242 Met Lys Trp Lys Xaa
      243             20
      246 <210> SEQ ID NO: 9
      247 <211> LENGTH: 21
      248 <212> TYPE: PRT
      249 <213> ORGANISM: synthetic construct
      251 <220> FEATURE:
      252 <221> NAME/KEY: MISC_FEATURE
      253 <222> LOCATION: (1)..(1)
      254 <223> OTHER INFORMATION: X is acetylated Lysine.
      257 <220> FEATURE:
      258 <221> NAME/KEY: MISC_FEATURE
      259 <222> LOCATION: (21)..(21)
      260 <223> OTHER INFORMATION: X is amidated Lysine.
      263 <400> SEQUENCE: 9
W--> 265 Xaa Ile Trp Phe Gln Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg
      266 1               5                   10                  15
      269 Met Lys Trp Lys Xaa
      270             20
      273 <210> SEQ ID NO: 10
      274 <211> LENGTH: 8
      275 <212> TYPE: PRT
      276 <213> ORGANISM: synthetic construct
      278 <220> FEATURE:
      279 <221> NAME/KEY: MISC_FEATURE
      280 <222> LOCATION: (8)..(8)
      281 <223> OTHER INFORMATION: X is amidated Lysine
      284 <400> SEQUENCE: 10
W--> 286 Asn Arg Arg Met Lys Trp Lys Xaa
      287 1               5
```

RAW SEQUENCE LISTING   DATE: 04/27/2007
PATENT APPLICATION: US/10/554,372   TIME: 11:42:58

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272007\J554372.raw

290 <210> SEQ ID NO: 11
291 <211> LENGTH: 42
292 <212> TYPE: PRT
293 <213> ORGANISM: human
295 <400> SEQUENCE: 11
297 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
298 1   5   10   15
301 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
302   20   25   30 .
305 Gly Leu Met Val Gly Gly Val Val Ile Ala
306   35   40

```
RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 04/27/2007
PATENT APPLICATION:   US/10/554,372       TIME: 11:42:59

                 Input Set : A:\PTO.KD.txt
                 Output Set: N:\CRF4\04272007\J554372.raw
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the
<220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:1; Xaa Pos. 1,2,6,7
Seq#:2; Xaa Pos. 2,3,5,7,8
Seq#:3; Xaa Pos. 1,2,6,7
Seq#:4; Xaa Pos. 16
Seq#:5; Xaa Pos. 1,5
Seq#:6; Xaa Pos. 21
Seq#:7; Xaa Pos. 1,16
Seq#:8; Xaa Pos. 1,21
Seq#:9; Xaa Pos. 1,21
Seq#:10; Xaa Pos. 8
```

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes
spaces.

```
Seq#:1; Line(s) 27,35,42
Seq#:3; Line(s) 108,116,117,124
```

VERIFICATION SUMMARY   DATE: 04/27/2007
PATENT APPLICATION: US/10/554,372   TIME: 11:42:59

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272007\J554372.raw

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16
L:215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
M:341 Repeated in SeqNo=8
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
```